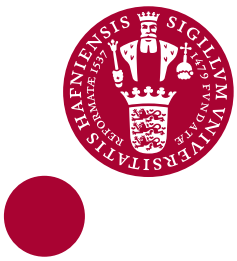

Transcriptional investigation of murine dendritic cells upon stimulation with the probiotics lactobacillus acidophilus NCFM and bifidobacterium bifido Z9

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In vivo, B-GOS significantly increased the numbers of beneficial bacteria, especially bifidobacteria, at the expense of less beneficial groups compared to the baseline and placebo. Significant increases in phagocytosis, NK cell activity and the production of anti-inflammatory cytokine,IL-10, and significant reduction in the production of pro-inflammatory (IL-6, IL-1b and TNF-a) cytokines were also observed. .
Discussion
B-GOS administration to healthy elderly persons resulted in positive effects on both the microflora composition and the immune response. The immunomodulatory effect should not be solely attributed to the achieved microflora change, since the specific oligosaccharide mixture showed a direct immunomodulatory effect against TNF-a mediated inflammation in vitro.

ERNA/DSM NUTRITIONAL PRODUCTS "SCIENTIFIC ASPECTS OF THE SUBSTANTIATION OF FUNCTIONAL FOOD BENEFITS WITHIN THE EU REGULATORY FRAMEWORK" (keynote)

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Key Words:

Regulation 1924/2006 on nutrition and health claims requires pre-market approval of any claim. The basic requirement is that all "nutrition and health claims shall be based on and substantiated by generally accepted scientific evidence." More concrete requirements on how to substantiate claims are found in the implementation Regulation 353/2008 and the EFSA guidance to applicants of July 2007, e.g. that the substantiation of health claims shall take into account the totality of the available scientific data and, by weighing the evidence, shall demonstrate the extent to which a claimed effect of the food is beneficial (and relevant) for the health of the intended target population. By mid April 2009 more than 50 EFSA opinions have been published. The vast majority of applications have been rejected, mainly because according to EFSA insufficient evidence had been presented to establish a cause-effect relationship. By taking such "yes or no" decisions, the extent to which a cause-effect relationship has been established is not reflected. It is questionable if such an approach is proportionate for all claims in the area of nutritional science. After all, the contribution of a food ingredient to human health should be judged by the 'totality of evidence', which is mechanistic data, epidemiological findings as well as human intervention studies. In human nutrition the ideal gold standard evidence might simply not always be reachable as e.g. studies in healthy people require a large sample size, long-term follow-up, high compliance and controlling for many lifestyle factors which are hardly possible to undertake and may not even be necessary in many cases. Also it appears that the project "Process for the Assessment of Scientific Support for Claims on Foods" (PASSCLAIM) which developed a generic tool to assess the scientific support for health claims for foods, has become the 'gold-standard' for scientific substantiations of claims. However, PASSCLAIM describes technologies and biomarkers which were top of the art at least six years ago. It did not consider new technologies used in nutrition research today, such as those giving access to holistics discovery of efficacy biomarkers namely genomics, transcriptomics, proteomics and metabolomics. In addition, imaging technologies (e.g., MRI etc) which are routinely used in medicine and which are quite advanced could be used to demonstrate efficacy of food ingredients, yet they are largely unknown to the nutritional community. It is conceivable to consider such technologies as appropriate as well in the substantiation of claims (i.e. imaging and brain function etc). In conclusion, the scientific opinions published by EFSA sofar lack a 'grading' which would better reflect the totality of evidence for a given ingredient. Finally, new emerging technologies should be explored as to there potential to better capture the subtle changes food ingredients may elicit to human physiology / metabolism which contribute to human health.

TRANSCRIPTIONAL INVESTIGATION OF MURINE DENDRITIC CELLS UPON STIMULATION WITH THE PROBIOTICS LACTOBACILLUS ACIDOPHILUS NCFM AND BIFIDOBACTERIUM BIFIDO Z9

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Key Words: Dendritic cells, Immune system, Lactobacillus acidophilus, Bifidobacterium Bifido

Introduction: Probiotic bacteria have the ability to influence our general health by interacting with immune cells located in the gut. Dendritic cells (DC) are of special relevance as they function as central gatekeepers and regulators of the immune response, invoked by orally ingested antigens, including the gut microbiota. The aim of this work was to elucidate the cytokine gene expression profile of murine DC upon in vitro stimulation with the probiotic strains

Lactobacillus acidophilus NCFM and Bifidobacterium bifido Z9.
Methods: Murine bone marrow derived DC were stimulated in vitro with Lactobacillus acidophilus NCFM and Bifidobacterium bifido Z9, respectively, and with both strains in combination. DC were harvested after 4 and 10 h of stimulation, RNA was extracted and reverse transcribed to cDNA. The expression of the genes encoding the pro-inflammatory cytokine IL-12 and the anti-inflammatory cytokine IL-10 was analysed by real-time PCR. Protein production was quantified by ELISA.
Results: The gene coding for IL-12 was strongly induced in both Lactobacillus acidophilus NCFM and Bifidobacterium bifido Z9 stimulated cells after 4 h. After 10 hours, Lactobacillus acidophilus NCFM stimulated cells still exhibited high IL-12 mRNA levels whereas they were strongly reduced in cells stimulated with Bifidobacterium bifido Z9. With both strains in a combination, the expression of the IL-12 gene was 45 % downregulated after 10 h compared to DC stimulated with Lactobacillus acidophilus NCFM alone. The gene encoding IL-10 was induced more than 2.5 times when both strains were used versus Lactobacillus acidophilus NCFM and Bifidobacterium bifido Z9 applied solely. Our results were verified by ELISA.
Discussion: It is indicated that Lactobacillus acidophilus NCFM and Bifidobacterium bifido Z9 differ in their capability to sustain stimulation or to provide an inhibitory signal leading to a faster reduction of IL-12 mRNA.

PROTEOMIC ANALYSIS OF HEPG2 CELLS IN RESPONSE TO THE TREATMENT OF ORIDONIN, AN ACTIVE CONSTITUENT OF THE MEDICINAL HERB ISODON RUBESCENS

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Key Words: Oridonin, Proteomics, HepG2 cells, Molecular mechanism

Oridonin, a diterpenoid compound, is the main active constituent of Isodon rubescens (Hemsl.) C.Y. Wu et Hsuan. Because of the remarkable effectiveness and low toxicity of I. rubescens, a lot of medicinal and functional food products have been developed based on I. rubescens. Pre-clinic and clinical investigations suggested that oridonin has antineoplastic property against a variety of cancers with high potency and low toxicity. However, the molecular mechanisms of oridonin have not been fully elucidated. To identify the molecular targets of oridonin in the treatment of hepatocarcinoma, we performed proteomic analysis of oridonin-treated HepG2 cells using two-dimensional gel electrophoresis coupled with MALDI-TOF MS/MS. Apoptosis and G2/M arrest were observed in HepG2 cells treated with 44 μM oridonin for 24 h. Proteomic analysis of the oridonin-treated cells revealed four differentially expressed proteins. Among them heat shock 70 kDa protein 1 (Hsp70.1), stress-induced-phosphoprotein 1 (Sti1), and glutathione reductase (GR) were upregulated; while poly(rC)-binding protein 1 (hnRNP-E1) was downregualted. Upregulation of Hsp70.1 promotes tumor necrosis factor (TNF) mediated apoptosis. Upregulation of GR promotes TNFR and FasL mediated apoptosis. Downregualtion of hnRNP–E1 reduces the translation of c-Myc and Bc1-2, and consequently induces apoptosis. Downregualtion of hnRNP–E1 may contribute to G2/M arrest via the reduced c-Myc synthesis, because in the absence of c-Myc the activity of cyclin-dependent kinases responsible for G2/M progression is reduced. Upregulation of Sti may also contribute to G2/M arrest by inhibiting the activity of cdc2 (one component of M-phase promoting factor) and the formation of 20S cyclosome complex (required for mitotic cyclin destruction and sister chromatid separation). In conclusion, this is the first time to demonstrate that upregulation of Hsp70.1, GR and Sti1 is responsible for the apoptotic effects, and upregulation of Sti1 and downregulation of hnRNP–E1 are responsible for the cell cycle arresting effects of oridonin in hepatocarcinorma HepG2 cells. (The work was supported by a grant, FRG/08-09/I-08, from Hong Kong Baptist University).

THE EVOLUTION OF HUMAN MICROFLORA IN CONNECTION WITH HUMAN DISEASES

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Key Words: GIT, intestinal bacteria, DNA hybridization, PCR, probiotics

The evolution of human intestinal microflora is closely connected with the health condition of human population. The symbiosis of eukaryotic and prokaryotic kingdoms present in the human body is a basis of our existance. The establishment of this state was developing over many centuries. The set of plagues in the history of humankind induced by pathogenic bacteria played the most important role in this grandiose evolutionary process. The balance between these kingdoms was disrupted in the second half of the 20th century due to ATB, drugs, pharmaceuticals and life style